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FIG. 1

Frequency of PAX5 α and β methylation in tumor cell line
primary tumors and non-malignant specimens

Sample Type	Samples Assayed	Number Methylated (%)		
		Alpha	Beta	Alpha + Beta
Breast				
Tumor Cell Lines	10	9 (90)	6 (60)	6 (60)
Tumors	30	21 (70)	15 (50)	11 (37)
Lung				
Tumor Cell Lines	11	9 (82)	6 (55)	6 (55)
Tumors				
ADC	25	16 (64)	13 (52)	10 (40) ^c
SCC	23	17 (74)	14 (61)	12 (52) ^c
Colon				
Tumors	42	9 (21) ^d	14 (33) ^d	4 (9.5)
BECs ^a	35	1 (2.9)	1 (2.9)	0 (0)
Sputum ^a	39	5 (13)	1 (2.6)	0 (0)
Blood lymphocytes ^b	20	0 (0)	0 (0)	0 (0)

^a Cancer-free heavy smokers

^b Cancer-free nonsmokers

^c $p=0.05$ for association of PAX5 α methylation to β methylation in lung tumors.

^d $p<0.0001$ as compared to methylation in lung or breast tumors.

FIG. 2

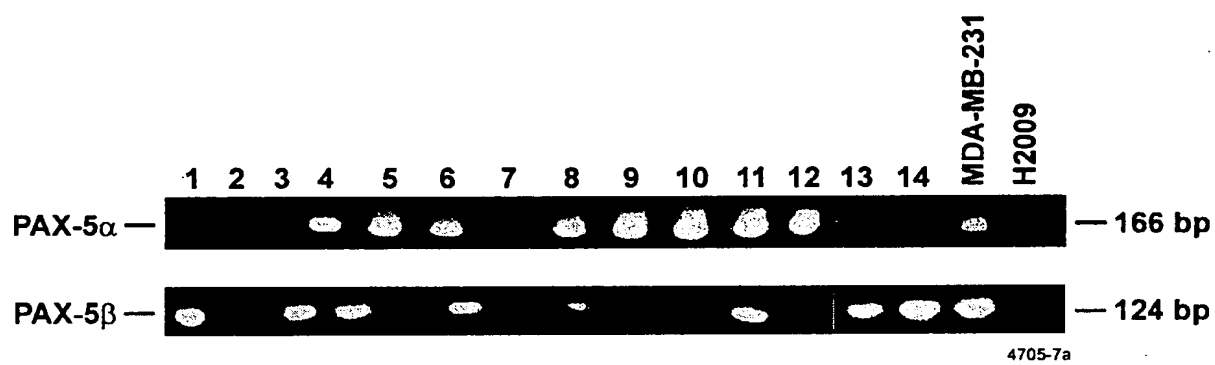


FIG.
3A.

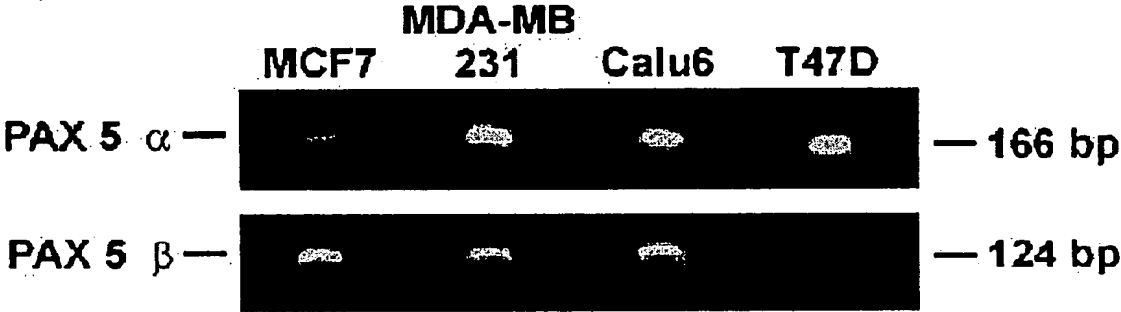
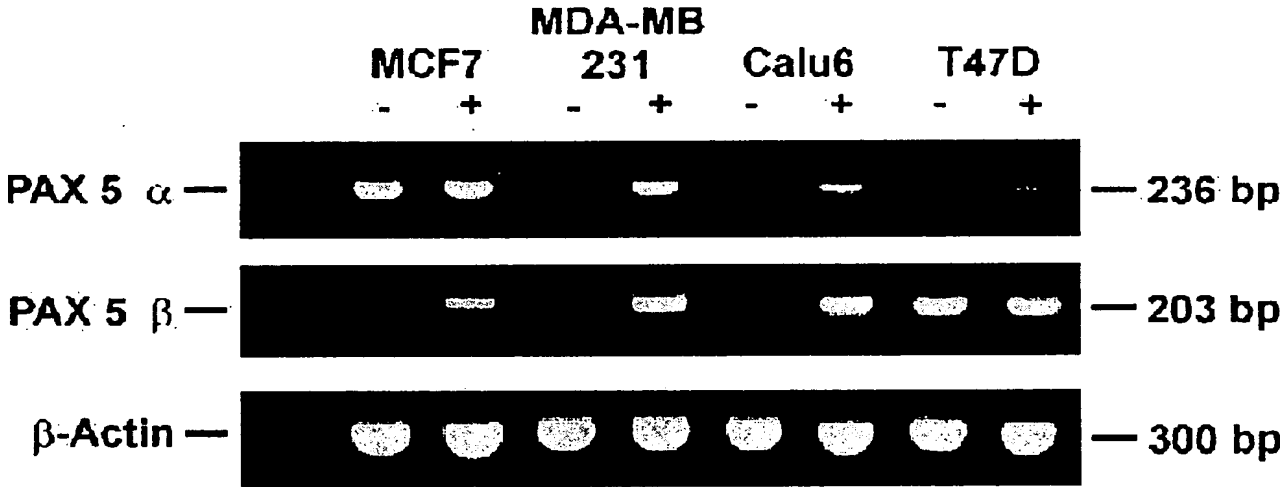


FIG.
3B.



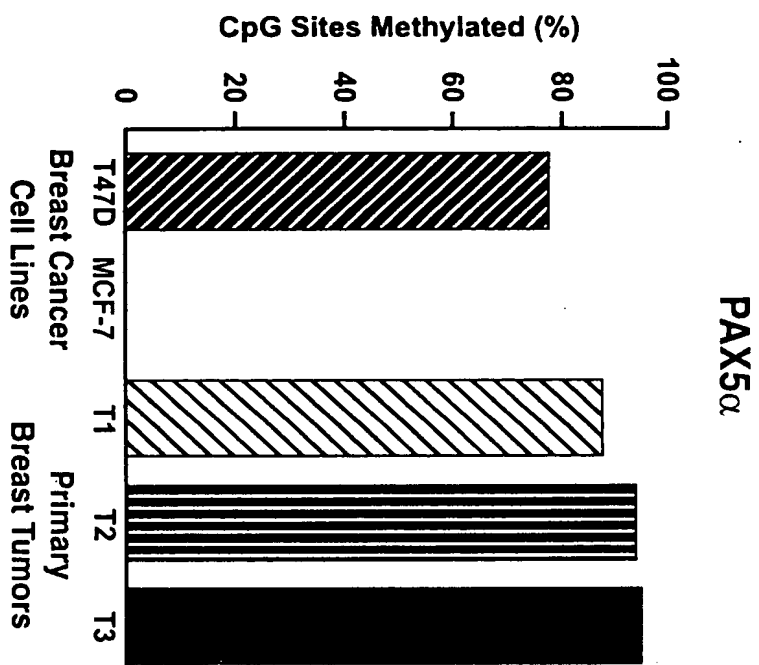


FIG. 4A

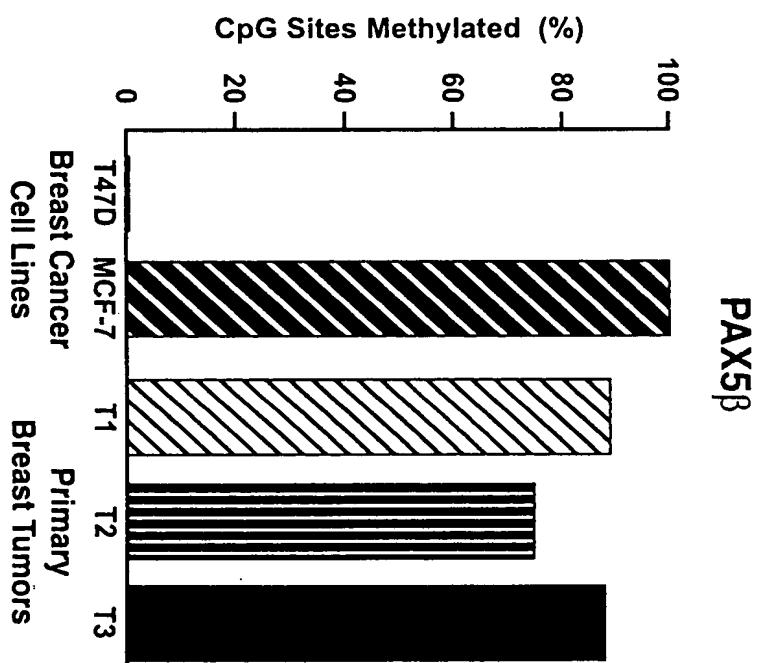


FIG. 4B

FIG. 5

Frequency of methylation of the Novel Helix Loop Helix Binding Protein, Novel Gene 2, and Beta3 genes in tumor cell lines, primary tumors and non-malignant specimens

Sample Type	HLHBP	Number Methylated (%)	
		Novel Gene 2	Beta 3
Breast			
Tumor Cell Lines	8/10 (80)	5/8 (63)	6/10 (60)
Tumors	ND	ND	6/15 (40)
Lung			
Tumor Cell Lines	8/11 (73)	1/7 (14)	1/12 (8)
Tumors			
ADC	ND	ND	11/21 (52)
SCC	13/22 (59)	ND	1/14 (7)
Blood lymphocytes ^a	0/11 (0)	0/11 (0)	0/11 (0)

HLHBP, helix loop helix binding protein, ADC, adenocarcinoma; SCC, squamous cell carcinoma; BECs, bronchial epithelial cells

^aCancer-free nonsmokers

ND, not determined